

#8

CRF Errors Corrected by the **ATC Systems Branch**CRF Processing Date: 10/22/01  
Edited by: mtt  
Verified by: \_\_\_\_\_Serial Number: 09/528225

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number input by applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. **ENTERED** The sequence numbers that were edited were \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: **RECEIVED**
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: **OCT 24 2001**
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at \_\_\_\_\_
- ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first O Action. DO NOT send a copy of this form.

RECEIVED

OCT 24 2001

TECH CENTER 1600/2900

1647

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/528,225

DATE: 10/22/2001

TIME: 11:21:36

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10222001\I528225.raw

ENTERED

5 <110> APPLICANT: Wang, Yi  
 6 Mueller, John  
 7 Matis, Louis A.  
 9 <120> TITLE OF INVENTION: Chimeric Proteins for Diagnosis and Treatment of Diabetes  
 11 <130> FILE REFERENCE: 109488-135  
 13 <140> CURRENT APPLICATION NUMBER: US 09/528,225  
 14 <141> CURRENT FILING DATE: 2000-03-21  
 16 <150> PRIOR APPLICATION NUMBER: PCT/US98/27408  
 17 <151> PRIOR FILING DATE: 1998-12-23  
 19 <150> PRIOR APPLICATION NUMBER: US 60/068,648  
 20 <151> PRIOR FILING DATE: 1997-12-23  
 22 <160> NUMBER OF SEQ ID NOS: 37  
 24 <170> SOFTWARE: PatentIn version 3.1  
 26 <210> SEQ ID NO: 1  
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 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Artificial Sequence ✓  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: IG1 Infusion Protein ✓  
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 42 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg  
 43 20 25 30  
 46 Arg Glu Ala Glu Asp Leu Asn Met Tyr Ala Met Met Ile Ala Arg Phe  
 47 35 40 45  
 50 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg  
 51 50 55 60  
 54 Leu Ile Ala Phe Thr Ser Glu Lys Cys Leu Glu Leu Ala Glu Tyr Leu  
 55 65 70 75 80  
 58 Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp Gly  
 59 85 90 95  
 62 Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser Leu  
 63 100 105 110  
 66 Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys Val  
 67 115 120 125  
 70 Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met Val  
 71 130 135 140  
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 75 145 150 155 160  
 79 <210> SEQ ID NO: 2  
 80 <211> LENGTH: 180  
 81 <212> TYPE: PRT  
 82 <213> ORGANISM: Artificial Sequence ✓  
 84 <220> FEATURE:  
 85 <223> OTHER INFORMATION: IG2 Fusion Protein ✓  
 89 <400> SEQUENCE: 2

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95 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
96          20          25          30
99 Arg Glu Ala Glu Asp Leu Met Asn Ile Leu Leu Gln Tyr Val Val Lys
100         35          40          45
103 Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe Lys Met Phe
104        50          55          60
107 Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala
108 65          70          75          80
111 Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu
112          85          90          95
115 Ala Glu Tyr Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met
116         100         105         110
119 Val Phe Asp Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile
120         115         120         125
123 Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg
124        130        135        140
127 Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly
128 145        150        155        160
131 Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn His His
132        165        170        175
135 His His His His
136        180
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141 <211> LENGTH: 144
142 <212> TYPE: PRT
143 <213> ORGANISM: Artificial Sequence ✓
145 <220> FEATURE:
146 <223> OTHER INFORMATION: IG3 Fusion Protein ✓
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156 Trp Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
157          20          25          30
160 Arg Glu Ala Glu Asp Leu Met Asn Ile Leu Leu Gln Tyr Val Val Lys
161          35          40          45
164 Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe Lys Met Phe
165          50          55          60
168 Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala
169 65          70          75          80
172 Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu
173          85          90          95
176 Ala Glu Tyr Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met
177         100         105         110
180 Val Phe Asp Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile
181         115         120         125
184 Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn His His His His His His
185        130        135        140

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189 <210> SEQ ID NO: 4
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191 <212> TYPE: PRT
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195 <223> OTHER INFORMATION: IG4 Fusion Protein ✓
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205 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
206 20 25 30
209 Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
210 35 40 45
213 Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
214 50 55 60
217 Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
218 65 70 75 80
221 Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp
222 85 90 95
225 Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
226 100 105 110
229 Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe
230 115 120 125
233 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
234 130 135 140
237 Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu
238 145 150 155 160
241 Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile His
242 165 170 175
245 His His His His His
246 180
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251 <211> LENGTH: 232
252 <212> TYPE: PRT
253 <213> ORGANISM: Artificial Sequence ✓
255 <220> FEATURE:
256 <223> OTHER INFORMATION: IG5 Fusion Protein ✓
260 <400> SEQUENCE: 5
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266 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
267 20 25 30
270 Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
271 35 40 45
274 Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
275 50 55 60
278 Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
279 65 70 75 80
282 Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp

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283          85          90          95
286 Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
287          100          105          110
290 Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe
291          115          120          125
294 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
295          130          135          140
298 Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu
299 145          150          155          160
302 Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly
303          165          170          175
306 Gly Gly Tyr Ile Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu
307          180          185          190
310 Arg Met Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met
311          195          200          205
314 Met Glu Tyr Gly Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys
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318 Val Asn His His His His His His
319 225          230
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328 <220> FEATURE:
329 <223> OTHER INFORMATION: IG6 Fusion Protein ✓
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339 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
340          20          25          30
343 Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
344          35          40          45
347 Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
348          50          55          60
351 Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
352 65          70          75          80
355 Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp
356          85          90          95
359 Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
360          100          105          110
363 Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe
364          115          120          125
367 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
368          130          135          140
371 Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu
372 145          150          155          160
375 Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly
376          165          170          175
379 Gly Gly Ile Glu His Asp Pro Arg Met Pro Ala Tyr Ile Ala Thr Gln

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380          180          185          190
383 Gly Pro Leu Ser His Thr Ile Ala Asp Phe Trp Gln Met Val Trp Glu
384          195          200          205
387 Ser Gly Cys Thr Val Ile Val Met Leu Thr Pro Leu Val Glu Asp Gly
388          210          215          220
391 Val Lys Gln Cys Asp Arg Tyr Trp Pro Asp Glu Gly Ala Ser Leu Tyr
392 225          230          235          240
395 His Val Tyr Glu Val Asn Leu Val Ser Glu His Ile Trp Cys Glu Asp
396          245          250          255
399 Phe Leu Val Arg Ser Phe Tyr Leu Lys Asn Val Gln Thr Gln Glu Thr
400          260          265          270
403 Arg Thr Leu Thr Gln Phe His Phe Leu Ser Trp Pro Ala Glu Gly Thr
404          275          280          285
407 Pro Ala Ser Thr Arg Pro Leu Leu Asp Phe Arg Arg Lys Val Asn Lys
408          290          295          300
411 Cys Tyr Arg Gly Arg Ser Cys Pro Ile Ile Val His Cys Ser Asp Gly
412 305          310          315          320
415 Ala Gly Arg Thr Gly Thr Tyr Ile Leu Ile Asp Met Val Leu Asn Arg
416          325          330          335
419 Met Ala Lys Gly Val Lys Glu Ile Asp Ile Ala Ala Thr Leu Glu His
420          340          345          350
423 Val Arg Asp Gln Arg Pro Gly Leu Val Arg Ser Lys Asp Gln Phe Glu
424          355          360          365
427 Phe Ala Leu Thr Ala Val Ala Glu Glu Val Asn Ala Ile Leu Lys Ala
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431 Leu Pro Gln His His His His His His
432 385          390
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437 <211> LENGTH: 444
438 <212> TYPE: PRT
439 <213> ORGANISM: Artificial Sequence ✓
441 <220> FEATURE:
442 <223> OTHER INFORMATION: IG7 Fusion Protein ✓
446 <400> SEQUENCE: 7
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453          20          25          30
456 Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
457          35          40          45
460 Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
461          50          55          60
464 Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
465 65          70          75          80
468 Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp
469          85          90          95
472 Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
473          100          105          110
476 Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe

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**VERIFICATION SUMMARY**

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